

SEQUENCE LISTING

<110> Sibley, David R.
Monsma, Frederick J.
Hamblin, Mark

<120> The ST-B17 Serotonin Receptor

<130> NIH047.1CP1C1

<140> unknown

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<150> US 08/428,242

<151> 1995-09-18

<160> 13

<170> FastSEQ for Windows Version 4.0

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<212> DNA

<213> primer

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 ctagccagga accccacccc catcttatgg catccccggg ggccctattc catcccaggg 180
 ctctcatcca gcccgaagct aactttcatt gactcgtcac atcagtaccc ctccccaac 240
 ttcttaccgg agtactccag gtggccctgc gtaggaggca cccctacaac tcctcccgat 300
 ctcttgaat cgctgctcga tgacctaaga accccgtttt gccaaacta ctctaagggtg 360
 cagcttcctt tctcctcctt tgccttcacc ctgtacctgc agtcaccata tcccgctcttg 420
 gtcctcaacc cagtcccc atg gtt cca gag cca ggc cct gtc aac agt agc 471

Met Val Pro Glu Pro Gly Pro Val Asn Ser Ser
 1 5 10

acc cca gcc tgg ggt ccc ggg cca ccg cct gct ccg ggg ggc agc ggc 519
 Thr Pro Ala Trp Gly Pro Gly Pro Pro Pro Ala Pro Gly Gly Ser Gly
 15 20 25

tgg gtg gct gcc gcg ctg tgc gtg gtc atc gtg ctg aca gca gcc gcc 567
 Trp Val Ala Ala Ala Leu Cys Val Val Ile Val Leu Thr Ala Ala Ala
 30 35 40

aat tcg ctg ctg atc gtg ctc att tgc acg cag ccc gcc gtg cgc aac 615
 Asn Ser Leu Leu Ile Val Leu Ile Cys Thr Gln Pro Ala Val Arg Asn
 45 50 55

acg tct aac ttc ttt ctg gtg tcg ctc ttc acg tcg gac ttg atg gtg 663
 Thr Ser Asn Phe Phe Leu Val Ser Leu Phe Thr Ser Asp Leu Met Val
 60 65 70 75

ggg ttg gtg gtg atg ccc cca gcc atg ctg aac gcg ctg tat ggg cgc 711
 Gly Leu Val Val Met Pro Pro Ala Met Leu Asn Ala Leu Tyr Gly Arg

tgg gtg tta gct cga ggc ctc tgt ctg ctt tgg act gcc ttc gac gtg	759
Trp Val Leu Ala Arg Gly Leu Cys Leu Leu Trp Thr Ala Phe Asp Val	
95 100 105	
atg tgc tgc agc gcc tcc atc ctc aac ctc tgc ctc atc agc ctg gac	807
Met Cys Cys Ser Ala Ser Ile Leu Asn Leu Cys Leu Ile Ser Leu Asp	
110 115 120	
cgc tac ctg ctc atc ctc tcg ccg ctg cgc tac aag ctg cgc atg aca	855
Arg Tyr Leu Leu Ile Leu Ser Pro Leu Arg Tyr Lys Leu Arg Met Thr	
125 130 135	
gcc ccg cga gcc ctg gcg ctc atc ctg ggt gcc tgg agc ctc gcg gcg	903
Ala Pro Arg Ala Leu Ala Leu Ile Leu Gly Ala Trp Ser Leu Ala Ala	
140 145 150 155	
ctt gcc tcc ttc cta ccc ctc ttg ctg ggc tgg cac gaa ctg ggc aaa	951
Leu Ala Ser Phe Leu Pro Leu Leu Leu Gly Trp His Glu Leu Gly Lys	
160 165 170	
gct cga aca cct gcc cct ggc cag tgc cgc cta ttg gcc agc ctg cct	999
Ala Arg Thr Pro Ala Pro Gly Gln Cys Arg Leu Leu Ala Ser Leu Pro	
175 180 185	
ttt gtc ctc gtg gcg tcc ggc gtc acc ttt ttc ctg cct tcg ggt gcc	1047
Phe Val Leu Val Ala Ser Gly Val Thr Phe Phe Leu Pro Ser Gly Ala	
190 195 200	
atc tgc ttc acc tac tgc agg atc ctt ctg gct gcc cgc aag cag gcg	1095
Ile Cys Phe Thr Tyr Cys Arg Ile Leu Leu Ala Ala Arg Lys Gln Ala	
205 210 215	
gtg caa gtg gcc tcg ctc acc acg ggc acg gct ggc cag gcc ttg gaa	1143
Val Gln Val Ala Ser Leu Thr Thr Gly Thr Ala Gly Gln Ala Leu Glu	
220 225 230 235	
acc ttg cag gtg ccc agg aca cca cgc cca ggg atg gag tcc gct gac	1191
Thr Leu Gln Val Pro Arg Thr Pro Arg Pro Gly Met Glu Ser Ala Asp	
240 245 250	
agt agg cgt ctg gcc acc aag cat agc agg aag gcc ttg aag gcc agc	1239
Ser Arg Arg Leu Ala Thr Lys His Ser Arg Lys Ala Leu Lys Ala Ser	
255 260 265	
ctg acc ctg ggc atc ctg ctg gga atg ttc ttt gtc acc tgg ctg ccc	1287
Leu Thr Leu Gly Ile Leu Leu Gly Met Phe Phe Val Thr Trp Leu Pro	
270 275 280	
ttc ttt gtg gcc aac ata gct cag gcc gtg tgt gac tgc atc tcc cca	1335
Phe Phe Val Ala Asn Ile Ala Gln Ala Val Cys Asp Cys Ile Ser Pro	
285 290 295	
ggc ctc ttc gat gtc ctc aca tgg ctg ggg tac tgt aat agc acc atg	1383

Gly Leu Phe Asp Val Leu Thr Trp Leu Gly Tyr Cys Asn Ser Thr Met
 300 305 310 315

aac cct atc atc tac ccg ctc ttt atg cgg gac ttc aag agg gcc ctg 1431
 Asn Pro Ile Ile Tyr Pro Leu Phe Met Arg Asp Phe Lys Arg Ala Leu
 320 325 330

ggc agg ttc ctg cat gcg tcc act gtc ccc cgg agc acc ggc cag ccc 1479
 Gly Arg Phe Leu His Ala Ser Thr Val Pro Arg Ser Thr Gly Gln Pro
 335 340 345

tgc ctc ccc ctc cat gtg gac ctc tca cag cgg tgc cag acc agg cct 1527
 Cys Leu Pro Leu His Val Asp Leu Ser Gln Arg Cys Gln Thr Arg Pro
 350 355 360

cag ctg cag cag gtg ctc gct ctg cct ctg ccg cca aac tca gat tca 1575
 Gln Leu Gln Gln Val Leu Ala Leu Pro Leu Pro Pro Asn Ser Asp Ser
 365 370 375

gac tcc gct tca ggg ggc acc tcg ggc ctg cag ctc aca gcc cag ctt 1623
 Asp Ser Ala Ser Gly Gly Thr Ser Gly Leu Gln Leu Thr Ala Gln Leu
 380 385 390 395

ctg ctg cct gga gag gcc aca cgg gac ccc ccg cca ccc acc agg gcc 1671
 Leu Leu Pro Gly Glu Ala Thr Arg Asp Pro Pro Pro Thr Arg Ala
 400 405 410

acc act gtg gtc aac ttc ttt gtc aca gac tct gtg gag cct gag ata 1719
 Thr Thr Val Val Asn Phe Phe Val Thr Asp Ser Val Glu Pro Glu Ile
 415 420 425

cgg ccg cat cca ctc agt tcc ccc gtg aac tgaccaggtc aagagctggc 1769
 Arg Pro His Pro Leu Ser Ser Pro Val Asn
 430 435

cattggaggc cacattcccg gagctctcag cccactctcc ctgagactag gaggtggtag 1829
 gtctcctgag agtgtgtctga attgaggtat ctcagctagc ccatcttctg ctgcagctcc 1889
 ttgactgagg ggtagtcaga cacat 1914

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 <212> PRT
 <213> Rat

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 35 40 45
 Val Leu Ile Cys Thr Gln Pro Ala Val Arg Asn Thr Ser Asn Phe Phe
 50 55 60
 Leu Val Ser Leu Phe Thr Ser Asp Leu Met Val Gly Leu Val Val Met
 65 70 75 80

Pro	Pro	Ala	Met	Leu	Asn	Ala	Leu	Tyr	Gly	Arg	Trp	Val	Leu	Ala	Arg
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Gly	Leu	Cys	Leu	Leu	Trp	Thr	Ala	Phe	Asp	Val	Met	Cys	Cys	Ser	Ala
			100					105					110		
Ser	Ile	Leu	Asn	Leu	Cys	Leu	Ile	Ser	Leu	Asp	Arg	Tyr	Leu	Leu	Ile
		115					120					125			
Leu	Ser	Pro	Leu	Arg	Tyr	Lys	Leu	Arg	Met	Thr	Ala	Pro	Arg	Ala	Leu
		130				135					140				
Ala	Leu	Ile	Leu	Gly	Ala	Trp	Ser	Leu	Ala	Ala	Leu	Ala	Ser	Phe	Leu
145					150					155					160
Pro	Leu	Leu	Leu	Gly	Trp	His	Glu	Leu	Gly	Lys	Ala	Arg	Thr	Pro	Ala
			165						170					175	
Pro	Gly	Gln	Cys	Arg	Leu	Leu	Ala	Ser	Leu	Pro	Phe	Val	Leu	Val	Ala
			180					185					190		
Ser	Gly	Val	Thr	Phe	Phe	Leu	Pro	Ser	Gly	Ala	Ile	Cys	Phe	Thr	Tyr
		195					200					205			
Cys	Arg	Ile	Leu	Leu	Ala	Ala	Arg	Lys	Gln	Ala	Val	Gln	Val	Ala	Ser
	210					215					220				
Leu	Thr	Thr	Gly	Thr	Ala	Gly	Gln	Ala	Leu	Glu	Thr	Leu	Gln	Val	Pro
225					230					235					240
Arg	Thr	Pro	Arg	Pro	Gly	Met	Glu	Ser	Ala	Asp	Ser	Arg	Arg	Leu	Ala
				245					250					255	
Thr	Lys	His	Ser	Arg	Lys	Ala	Leu	Lys	Ala	Ser	Leu	Thr	Leu	Gly	Ile
			260					265					270		
Leu	Leu	Gly	Met	Phe	Phe	Val	Thr	Trp	Leu	Pro	Phe	Phe	Val	Ala	Asn
		275					280					285			
Ile	Ala	Gln	Ala	Val	Cys	Asp	Cys	Ile	Ser	Pro	Gly	Leu	Phe	Asp	Val
	290					295					300				
Leu	Thr	Trp	Leu	Gly	Tyr	Cys	Asn	Ser	Thr	Met	Asn	Pro	Ile	Ile	Tyr
305					310					315					320
Pro	Leu	Phe	Met	Arg	Asp	Phe	Lys	Arg	Ala	Leu	Gly	Arg	Phe	Leu	His
			325						330					335	
Ala	Ser	Thr	Val	Pro	Arg	Ser	Thr	Gly	Gln	Pro	Cys	Leu	Pro	Leu	His
			340					345					350		
Val	Asp	Leu	Ser	Gln	Arg	Cys	Gln	Thr	Arg	Pro	Gln	Leu	Gln	Gln	Val
	355						360					365			
Leu	Ala	Leu	Pro	Leu	Pro	Pro	Asn	Ser	Asp	Ser	Asp	Ser	Ala	Ser	Gly
	370					375					380				
Gly	Thr	Ser	Gly	Leu	Gln	Leu	Thr	Ala	Gln	Leu	Leu	Leu	Pro	Gly	Glu
385					390					395					400
Ala	Thr	Arg	Asp	Pro	Pro	Pro	Pro	Thr	Arg	Ala	Thr	Thr	Val	Val	Asn
			405						410					415	
Phe	Phe	Val	Thr	Asp	Ser	Val	Glu	Pro	Glu	Ile	Arg	Pro	His	Pro	Leu
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 <212> DNA
 <213> Rat

<220>
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<221> intron

<222> (1312)...(1505)

<221> CDS

<222> (1506)...(1943)

<400> 9

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ctagccagga accccacccc catcttatgg catccccggt ggccctattc catcccaggg 180
ctctcatcca gcccacaagt aactttcatt gactcgtcac atcagtaccc ctccccaaac 240
ttcttaccgg agtactccag gtggccctgc gtaggaggca cccctacaac tctctccgat 300
ctcttgaaat cgctgtctga tgacctaaga accccgtttt gccaatata ctctaagggtg 360
cagcttcctt tctctcctt tgccttcacc ctgtacctgc agtcaccata tcccgtcttg 420
gtcctcaacc cagtcccc atg gtt cca gag cca ggc cct gtc aac agt agc 471
                Met Val Pro Glu Pro Gly Pro Val Asn Ser Ser
                  1             5             10
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acc cca gcc tgg ggt ccc ggg cca ccg cct gct ccg ggg ggc agc ggc 519
Thr Pro Ala Trp Gly Pro Gly Pro Pro Ala Pro Gly Gly Ser Gly
              15             20             25
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tgg gtg gct gcc gcg ctg tgc gtg gtc atc gtg ctg aca gca gcc gcc 567
Trp Val Ala Ala Ala Leu Cys Val Val Ile Val Leu Thr Ala Ala Ala
              30             35             40
```

```
aat tgc ctg ctg atc gtg ctc att tgc acg cag ccc gcc gtg cgc aac 615
Asn Ser Leu Leu Ile Val Leu Ile Cys Thr Gln Pro Ala Val Arg Asn
              45             50             55
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acg tct aac ttc ttt ctg gtg tgc ctc ttc acg tgc gac ttg atg gtg 663
Thr Ser Asn Phe Phe Leu Val Ser Leu Phe Thr Ser Asp Leu Met Val
              60             65             70             75
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ggg ttg gtg gtg atg ccc cca gcc atg ctg aac gcg ctg tat ggg cgc 711
Gly Leu Val Val Met Pro Pro Ala Met Leu Asn Ala Leu Tyr Gly Arg
              80             85             90
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tgg gtg tta gct cga ggc ctc tgt ctg ctt tgg act gcc ttc gac gtg 759
Trp Val Leu Ala Arg Gly Leu Cys Leu Leu Trp Thr Ala Phe Asp Val
              95             100             105
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atg tgc tgc agc gcc tcc atc ctc aac ctc tgc ctc atc agc ctg gac 807
Met Cys Cys Ser Ala Ser Ile Leu Asn Leu Cys Leu Ile Ser Leu Asp
              110             115             120
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cgc tac ctg ctc atc ctc tgc ccg ctg cgc tac aag ctg cgc atg aca 855
Arg Tyr Leu Leu Ile Leu Ser Pro Leu Arg Tyr Lys Leu Arg Met Thr
              125             130             135
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gcc ccg cga gcc ctg gcg ctc atc ctg ggt gcc tgg agc ctc gcg gcg 903
Ala Pro Arg Ala Leu Ala Leu Ile Leu Gly Ala Trp Ser Leu Ala Ala
              140             145             150             155
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ctt gcc tcc ttc cta ccc ctc ttg ctg ggc tgg cac gaa ctg ggc aaa 951
 Leu Ala Ser Phe Leu Pro Leu Leu Leu Gly Trp His Glu Leu Gly Lys
 160 165 170

gct cga aca cct gcc cct ggc cag tgc cgc cta ttg gcc agc ctg cct 999
 Ala Arg Thr Pro Ala Pro Gly Gln Cys Arg Leu Leu Ala Ser Leu Pro
 175 180 185

ttt gtc ctc gtg gcg tcc ggc gtc acc ttt ttc ctg cct tcg ggt gcc 1047
 Phe Val Leu Val Ala Ser Gly Val Thr Phe Phe Leu Pro Ser Gly Ala
 190 195 200

atc tgc ttc acc tac tgc agg atc ctt ctg gct gcc cgc aag cag gcg 1095
 Ile Cys Phe Thr Tyr Cys Arg Ile Leu Leu Ala Ala Arg Lys Gln Ala
 205 210 215

gtg caa gtg gcc tcg ctc acc acg ggc acg gct ggc cag gcc ttg gaa 1143
 Val Gln Val Ala Ser Leu Thr Thr Gly Thr Ala Gly Gln Ala Leu Glu
 220 225 230 235

acc ttg cag gtg ccc agg aca cca cgc cca ggg atg gag tcc gct gac 1191
 Thr Leu Gln Val Pro Arg Thr Pro Arg Pro Gly Met Glu Ser Ala Asp
 240 245 250

agt agg cgt ctg gcc acc aag cat agc agg aag gcc ttg aag gcc agc 1239
 Ser Arg Arg Leu Ala Thr Lys His Ser Arg Lys Ala Leu Lys Ala Ser
 255 260 265

ctg acc ctg ggc atc ctg ctg gga atg ttc ttt gtc acc tgg ctg ccc 1287
 Leu Thr Leu Gly Ile Leu Leu Gly Met Phe Phe Val Thr Trp Leu Pro
 270 275 280

ttc ttt gtg gcc aac ata gct cag gtaaaatgat gaccgtgaag gtgggatgag 1341
 Phe Phe Val Ala Asn Ile Ala Gln
 285 290

cttagggtctg accggagaga cgccatgctt cactgggcaa aggtgggagg gaggaggatg 1401
 gctcatctgt ggtgcctgtg tctgtgtttc tgtcctatcc ctgctgggtg ggtagcctgg 1461
 gtcctgctt gggacatggg gtgtgatgag tcttatctcc acag gcc gtg tgt gac 1517
 Ala Val Cys Asp
 295

tgc atc tcc cca ggc ctc ttc gat gtc ctc aca tgg ctg ggg tac tgt 1565
 Cys Ile Ser Pro Gly Leu Phe Asp Val Leu Thr Trp Leu Gly Tyr Cys
 300 305 310

aat agc acc atg aac cct atc atc tac ccg ctc ttt atg cgg gac ttc 1613
 Asn Ser Thr Met Asn Pro Ile Ile Tyr Pro Leu Phe Met Arg Asp Phe
 315 320 325

aag agg gcc ctg ggc agg ttc ctg cat gcg tcc act gtc ccc cgg agc 1661
 Lys Arg Ala Leu Gly Arg Phe Leu His Ala Ser Thr Val Pro Arg Ser
 330 335 340

acc ggc cag ccc tgc ctc ccc ctc cat gtg gac ctc tca cag cgg tgc 1709
 Thr Gly Gln Pro Cys Leu Pro Leu His Val Asp Leu Ser Gln Arg Cys
 345 350 355

cag acc agg cct cag ctg cag cag gtg ctc gct ctg cct ctg ccg cca 1757
 Gln Thr Arg Pro Gln Leu Gln Gln Val Leu Ala Leu Pro Leu Pro Pro
 360 365 370 375

aac tca gat tca gac tcc gct tca ggg ggc acc tcg ggc ctg cag ctc 1805
 Asn Ser Asp Ser Asp Ser Ala Ser Gly Gly Thr Ser Gly Leu Gln Leu
 380 385 390

aca gcc cag ctt ctg ctg cct gga gag gcc aca cgg gac ccc ccg cca 1853
 Thr Ala Gln Leu Leu Leu Pro Gly Glu Ala Thr Arg Asp Pro Pro Pro
 395 400 405

ccc acc agg gcc acc act gtg gtc aac ttc ttt gtc aca gac tct gtg 1901
 Pro Thr Arg Ala Thr Thr Val Val Asn Phe Phe Val Thr Asp Ser Val
 410 415 420

gag cct gag ata cgg ccg cat cca ctc agt tcc ccc gtg aac 1943
 Glu Pro Glu Ile Arg Pro His Pro Leu Ser Ser Pro Val Asn
 425 430 435

tgaccagggtc aagagctggc cattggaggc cacattcccg gagctctcag cccactctcc 2003
 ctgagactag gaggtggtag gtctcctgag agtgtgctga attgaggtat ctcagctagc 2063
 ccattcttctg ctgcagctcc ttgactgagg ggtagtcaga cacat 2108

<210> 10
 <211> 291
 <212> PRT
 <213> Rat

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 35 40 45
 Val Leu Ile Cys Thr Gln Pro Ala Val Arg Asn Thr Ser Asn Phe Phe
 50 55 60
 Leu Val Ser Leu Phe Thr Ser Asp Leu Met Val Gly Leu Val Val Met
 65 70 75 80
 Pro Pro Ala Met Leu Asn Ala Leu Tyr Gly Arg Trp Val Leu Ala Arg
 85 90 95
 Gly Leu Cys Leu Leu Trp Thr Ala Phe Asp Val Met Cys Cys Ser Ala
 100 105 110
 Ser Ile Leu Asn Leu Cys Leu Ile Ser Leu Asp Arg Tyr Leu Leu Ile
 115 120 125
 Leu Ser Pro Leu Arg Tyr Lys Leu Arg Met Thr Ala Pro Arg Ala Leu
 130 135 140
 Ala Leu Ile Leu Gly Ala Trp Ser Leu Ala Ala Leu Ala Ser Phe Leu
 145 150 155 160
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<221> misc_feature
 <222> (1)...(1647)
 <223> n = A,T,C or G

<400> 12

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 caccctcggt cctc atg gtc cca gag ccg ggc cca acc gcc aat agc acc 170
 Met Val Pro Glu Pro Gly Pro Thr Ala Asn Ser Thr
 1 5 10

ccg gcc tgg ggg gca ggc gcc cgt cgn nng ggg ggc agc ggc tgg gtg 218
 Pro Ala Trp Gly Ala Gly Ala Arg Arg Xaa Gly Gly Ser Gly Trp Val
 15 20 25

gcg gcc ggc ctg tgc gtg gtc atc gcg ctg acg gcg gcg gcc aac tcg 266
 Ala Ala Gly Leu Cys Val Val Ile Ala Leu Thr Ala Ala Ala Asn Ser
 30 35 40

ctg ctg atc gcg ctc atc tgc act cag ccc gcg ctg cgc aac acg tcc 314
 Leu Leu Ile Ala Leu Ile Cys Thr Gln Pro Ala Leu Arg Asn Thr Ser
 45 50 55 60

aac ttc ttc ctg gtg tgc ctc ttc acg tct gac ctg atg gtc ggg ctg 362
 Asn Phe Phe Leu Val Ser Leu Phe Thr Ser Asp Leu Met Val Gly Leu
 65 70 75

gtg gtg atg ccg ccg gcc atg ctg aac gcg ctg tac ggg cgc tgg gtg 410
 Val Val Met Pro Pro Ala Met Leu Asn Ala Leu Tyr Gly Arg Trp Val
 80 85 90

ctg gcg cgc ggc ctc tgc ctg ctc tgg acc gcc ttc gac gtg atg tgc 458
 Leu Ala Arg Gly Leu Cys Leu Leu Trp Thr Ala Phe Asp Val Met Cys
 95 100 105

tgc agc gcc tcc atc ctc aac ctc tgc ctc atc agc ctg gac cgc tac 506
 Cys Ser Ala Ser Ile Leu Asn Leu Cys Leu Ile Ser Leu Asp Arg Tyr
 110 115 120

ctg ctc atc ctc tgc ccg ctg cgc tac aag ctg cgc atg acg ccc ctg 554
 Leu Leu Ile Leu Ser Pro Leu Arg Tyr Lys Leu Arg Met Thr Pro Leu
 125 130 135 140

cgt gcc ctg gcc cta gtc ctg ggc ggc tgg agc ctc gcc gct ctc gcc 602
 Arg Ala Leu Ala Leu Val Leu Gly Gly Trp Ser Leu Ala Ala Leu Ala
 145 150 155

tcc ttc ctg ccc ctg ctg ctg ggc tgg cac gag ctg ggc cac gca cgg 650
 Ser Phe Leu Pro Leu Leu Leu Gly Trp His Glu Leu Gly His Ala Arg
 160 165 170

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 Pro Pro Val Pro Gly Gln Cys Arg Leu Leu Ala Ser Leu Pro Phe Val
 175 180 185

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Leu Val Ala Ser Gly Leu Thr Phe Phe Leu Pro Ser Gly Ala Ile Cys	
190 195 200	
ttc acc tac tgc agg atc ctg cta gct gcc cgc aag cag gcc gtg cag	794
Phe Thr Tyr Cys Arg Ile Leu Leu Ala Ala Arg Lys Gln Ala Val Gln	
205 210 215 220	
gtg gcc tcc ctc acc acc ggc atg gcc agt cag gcc tcg gag acg ctg	842
Val Ala Ser Leu Thr Thr Gly Met Ala Ser Gln Ala Ser Glu Thr Leu	
225 230 235	
cag gta ccc agg agc cca gcg gca ggg gtg gag tct gct gac agc agg	890
Gln Val Pro Arg Ser Pro Ala Ala Gly Val Glu Ser Ala Asp Ser Arg	
240 245 250	
cgt cta gca acg aag agc agc agg aag ggc ctg aag gcc agc atg acg	938
Arg Leu Ala Thr Lys Ser Ser Arg Lys Gly Leu Lys Ala Ser Met Thr	
255 260 265	
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Leu Gly Ile Leu Leu Gly Met Phe Phe Val Thr Trp Leu Pro Phe Phe	
270 275 280	
gtg gcc aac ata gtc cag gcc gtg tgc gac tgc atc tcc cca ggc ctc	1034
Val Ala Asn Ile Val Gln Ala Val Cys Asp Cys Ile Ser Pro Gly Leu	
285 290 295 300	
ttc gat gtc ctc aca tgg ctg ggt tac tgt aac agc acc atg aac ccc	1082
Phe Asp Val Leu Thr Trp Leu Gly Tyr Cys Asn Ser Thr Met Asn Pro	
305 310 315	
atc atc tac cca ctc ttc atg ctg gac ttc aag cgg gcg ctg ggc agg	1130
Ile Ile Tyr Pro Leu Phe Met Leu Asp Phe Lys Arg Ala Leu Gly Arg	
320 325 330	
ttc ctg cca tgt cca cgc tgt ccc cgg gag ccc agg cca gcc tgg cct	1178
Phe Leu Pro Cys Pro Arg Cys Pro Arg Glu Pro Arg Pro Ala Trp Pro	
335 340 345	
cgc cat cac tgc gca cct ctc aca gcg gcc ccc ggc ccg gcc tta gcc	1226
Arg His His Cys Ala Pro Leu Thr Ala Ala Pro Gly Pro Ala Leu Ala	
350 355 360	
tac agc agg tgc tgc cgc tgc ccc tgc cgc cgg act cag att cgg act	1274
Tyr Ser Arg Cys Cys Arg Cys Pro Cys Arg Arg Thr Gln Ile Arg Thr	
365 370 375 380	
cag acg cag gct cag gcg gct cct cgg gcg tgc ggc tca cgg ccc agc	1322
Gln Thr Gln Ala Gln Ala Ala Pro Arg Ala Cys Gly Ser Arg Pro Ser	
385 390 395	
tgc tgc ttc ctg gcg agg cca ccc agg acc ccc cgc tgc cca cca ggg	1370
Cys Cys Phe Leu Ala Arg Pro Pro Arg Thr Pro Arg Cys Pro Pro Gly	

400

405

410

ccg ctg ccg ccg tca att tct tca aca tcg sac ccc gcg gag ccc gag 1418
 Pro Leu Pro Pro Ser Ile Ser Ser Thr Ser Xaa Pro Ala Glu Pro Glu
 415 420 425

ctg cgg ccg cat cca ctt ggc atc ccc acg aac tga cccggcttgg 1464
 Leu Arg Pro His Pro Leu Gly Ile Pro Thr Asn *
 430 435

ggctggccaa tggggagctg gattgagcag aaccagacc ctgagtcctt gggccagctc 1524
 ttggctaaga ccaggaggct gcaagtctcc tagaagccct ctgagctcca gaggggtgcg 1584
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 aga 1647

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 <213> Homo sapiens

<220>
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 <223> Xaa = Any Amino Acid

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 20 25 30
 Cys Val Val Ile Ala Leu Thr Ala Ala Ala Asn Ser Leu Leu Ile Ala
 35 40 45
 Leu Ile Cys Thr Gln Pro Ala Leu Arg Asn Thr Ser Asn Phe Phe Leu
 50 55 60
 Val Ser Leu Phe Thr Ser Asp Leu Met Val Gly Leu Val Val Met Pro
 65 70 75 80
 Pro Ala Met Leu Asn Ala Leu Tyr Gly Arg Trp Val Leu Ala Arg Gly
 85 90 95
 Leu Cys Leu Leu Trp Thr Ala Phe Asp Val Met Cys Cys Ser Ala Ser
 100 105 110
 Ile Leu Asn Leu Cys Leu Ile Ser Leu Asp Arg Tyr Leu Leu Ile Leu
 115 120 125
 Ser Pro Leu Arg Tyr Lys Leu Arg Met Thr Pro Leu Arg Ala Leu Ala
 130 135 140
 Leu Val Leu Gly Gly Trp Ser Leu Ala Ala Leu Ala Ser Phe Leu Pro
 145 150 155 160
 Leu Leu Leu Gly Trp His Glu Leu Gly His Ala Arg Pro Pro Val Pro
 165 170 175
 Gly Gln Cys Arg Leu Leu Ala Ser Leu Pro Phe Val Leu Val Ala Ser
 180 185 190
 Gly Leu Thr Phe Phe Leu Pro Ser Gly Ala Ile Cys Phe Thr Tyr Cys
 195 200 205
 Arg Ile Leu Leu Ala Ala Arg Lys Gln Ala Val Gln Val Ala Ser Leu
 210 215 220
 Thr Thr Gly Met Ala Ser Gln Ala Ser Glu Thr Leu Gln Val Pro Arg

225					230					235				240	
Ser	Pro	Ala	Ala	Gly	Val	Glu	Ser	Ala	Asp	Ser	Arg	Arg	Leu	Ala	Thr
				245					250					255	
Lys	Ser	Ser	Arg	Lys	Gly	Leu	Lys	Ala	Ser	Met	Thr	Leu	Gly	Ile	Leu
			260					265					270		
Leu	Gly	Met	Phe	Phe	Val	Thr	Trp	Leu	Pro	Phe	Phe	Val	Ala	Asn	Ile
		275					280					285			
Val	Gln	Ala	Val	Cys	Asp	Cys	Ile	Ser	Pro	Gly	Leu	Phe	Asp	Val	Leu
	290					295					300				
Thr	Trp	Leu	Gly	Tyr	Cys	Asn	Ser	Thr	Met	Asn	Pro	Ile	Ile	Tyr	Pro
305					310					315					320
Leu	Phe	Met	Leu	Asp	Phe	Lys	Arg	Ala	Leu	Gly	Arg	Phe	Leu	Pro	Cys
				325					330					335	
Pro	Arg	Cys	Pro	Arg	Glu	Pro	Arg	Pro	Ala	Trp	Pro	Arg	His	His	Cys
			340					345					350		
Ala	Pro	Leu	Thr	Ala	Ala	Pro	Gly	Pro	Ala	Leu	Ala	Tyr	Ser	Arg	Cys
		355					360					365			
Cys	Arg	Cys	Pro	Cys	Arg	Arg	Thr	Gln	Ile	Arg	Thr	Gln	Thr	Gln	Ala
	370					375					380				
Gln	Ala	Ala	Pro	Arg	Ala	Cys	Gly	Ser	Arg	Pro	Ser	Cys	Cys	Phe	Leu
385					390					395					400
Ala	Arg	Pro	Pro	Arg	Thr	Pro	Arg	Cys	Pro	Pro	Gly	Pro	Leu	Pro	Pro
				405					410					415	
Ser	Ile	Ser	Ser	Thr	Ser	Xaa	Pro	Ala	Glu	Pro	Glu	Leu	Arg	Pro	His
			420					425					430		
Pro	Leu	Gly	Ile	Pro	Thr	Asn									
		435													